

# FIGURE 1A

|     |             |            |             |            |            |             |             |             |            |              |
|-----|-------------|------------|-------------|------------|------------|-------------|-------------|-------------|------------|--------------|
| 1   | GAATTTGGCC  | CTCGAGGCCA | AGAAATTCGGC | ACGAGGCGCG | GCGCCACGCG | CAGGCAGAGC  | GCTGTGCGCAT | CCCGGCGGTC  | CACCCGCCAT | GGGGCTCTCC   |
| 1   | CTTAAACCGG  | GAGCTCCGGT | TCCTTAAGCCG | TGCTCCGGC  | CGCGGTGCG  | GTCCGTCTCG  | CGACAGCGTA  | GGGCCGCGAG  | GTGGCGGTA  | CCCCGAGAGG   |
|     |             |            |             |            |            |             |             |             | Me         | tglyLeuSer   |
| 101 | TGGAGCCCGC  | GACCTCCACT | GCTGATGATC  | CTGCTACTGG | TGCTGTCTGT | GTGGCTGCCA  | CTTTGGAGCAG | GAACCTCCCT  | TGCCACAGAG | AACAGGTTTG   |
|     | ACCTCGGCG   | CTGGAGGTGA | CGACTACTAG  | GACGATGACC | ACGACAGCAA | CACCGACGGT  | GAACCTCGTC  | CTTTGAGGGA  | ACGGTGTCTC | TTGTCCAAAC   |
| 5   | TrpSerProA  | rgProProLe | uLeuMetIle  | LeuLeuLeuV | alleuSerLe | uTrpLeuPro  | LeuGlyAlaG  | lyAsnSerLe  | uAlaThrGlu | AsnArgPheVal |
| 201 | TGAACAGCTG  | TACCCAGGCC | AGAAAGAAAT  | GCGAGGCTAA | TCCCGTTGTC | AAGGTGCTCT  | ACCAGACCTT  | GGGCTCTGTC  | ACCTCCAGTT | TAAGCAGGCC   |
|     | ACTTGTGAC   | ATGGGTCCGG | TCTTTCTTTA  | CGCTCCGATT | AGGGGAACG  | TTCCGACGGA  | TGGTCTGGA   | CCCCGAGACG  | TGGAGGTCAA | ATTCTGCCGG   |
| 39  | AsnSerCy    | sThrGlnAla | ArgLysLysC  | ysGluAlaAs | nProAlaCys | LysAlaAlaT  | yrGlnHisLe  | uGlySerCys  | ThrSerSerL | euSerArgPro  |
| 301 | GCTGCCCTTA  | GAGGAGTCTG | CCATGTCTGC  | AGACTGCCTA | GAGGCAGCAG | AACAACTCAG  | GAACAGCTCT  | CTGATAGACT  | GCAGGTGCCA | TCGGCGCATG   |
|     | CGACGGGAAT  | CTCCTCAGAC | GGTACAGACG  | TCTGACGGAT | CTCCGTCTGC | TTGTGTGAGTC | CTTTGTCGAGA | GACTATCTGA  | CGTCCACGGT | AGCCGCGTAC   |
| 72  | LeuProLeu   | GluGluSera | laMetSerAl  | aAspCysLeu | GluAlaAlaG | luGlnLeuAr  | gAsnSerSer  | LeulleAspC  | ysArgCysHi | sArgargMet   |
| 401 | AAGCACAAG   | CTACCTGTCT | GGACATTTAT  | TGGACCGTTC | ACCCTGCCCG | AAGCCTTGGT  | GACTACGAGT  | TGGATGTCTC  | ACCTATATGA | GACACACTGA   |
|     | TTCTGTGTTTC | GATGGACAGA | CCTGTAAATA  | ACCTGGCAAG | TGGGACGGC  | TTCCGAACCA  | CTGATGCTCA  | ACCTACAGAG  | TGGGATACTT | CTGTGTCACT   |
| 105 | LysHisGlnA  | laThrCysLe | uAspIleTyr  | TrpThrValH | isProAlaAr | gSerLeuGly  | AspTyrGluL  | euAspValSe  | rProTyrGlu | AspThrValThr |
| 501 | CCAGCAAAAC  | CTGGAAAATG | AATCTTAGCA  | AGTTGAACAT | GCTCAAACCA | GACTCGGACC  | TCTGCCTCAA  | ATTTGCTATG  | CTGTGTACTC | TTCACGACAA   |
|     | GGTCGTTTGG  | GACCTTTTAC | TTAGAACTGT  | TCAACTTTGT | CGAGTTTGGT | CTGAGCCTGG  | AGACGAGATT  | TAAACGATAC  | GACACATGAG | AAGTGTGTGT   |
| 139 | SerLysPr    | oTrpLysMet | AsnLeuSerL  | ysLeuAsnMe | tLeuLysPro | AspSerAspL  | euCysLeuLy  | sPheAlaMet  | LeuCysThrL | euHisAspLys  |
| 601 | GTGTGACCGC  | CTGCGCAAGG | CCTACGGGGA  | GGCATGCTCA | GGATCCGCT  | GCCAGCGCCA  | CCTCTGCCCTA | GCCCAGCTGC  | GCTCCTTCTT | TGAGAAGGCA   |
|     | CACACTGGCG  | GACGGGTTCC | GGATGCCCTT  | CCGTACGAGT | CCCTAGGCGA | CGGTCCGGT   | GGAGACGGAT  | CGGTCTGACG  | CGAGGAAGAA | ACTCTTCCGT   |
| 172 | CysAspArg   | LeuArgLysA | laTyrGlyG   | uAlaCysSer | GlyIleArgC | ysGlnArgHi  | sLeuCysLeu  | AlaGlnLeuA  | rgSerPhePh | eGluLysAla   |
| 701 | GCAGAGTCCC  | ACGCTCAGGG | TCTGTCTGCTG | TGTCCCTGTG | CACCAGAAGA | TGCGGGCTGT  | GGGAGGGGC   | GGCGTAACAC  | CATCGCCCCC | AGTTGGGCCC   |
|     | CGTCTCAGGG  | TGCGAGTCCC | AGACGACGAC  | ACAGGACAC  | GTGCTCTTCT | ACGCCGACA   | CCCCTCGCCG  | CCGCAATTGTG | GTAGCGGGG  | TCAACGCGGG   |
| 205 | AlaGluSerH  | isAlaGlnG  | lLeuLeuLeu  | CysProCysA | laProGluAs | pAlaGlyCys  | GlyGluArgA  | rgArgAsnTh  | rIleAlaPro | SerCysAlaLeu |
| 801 | TGCCCTTCTGT | AACCCCAAT  | TGCCCTGGATC | TGCGGAGCTT | CTGCCGTGCG | GACCCCTTGT  | GCAGATCACC  | CCTGATGGAC  | TTCCAGACCC | ACTGTCTATCC  |
|     | ACGGAAGACA  | TTGGGGTTA  | ACGGACCTAG  | ACGCCCTGAA | GACGGACGCG | CTGGGAACA   | CGTCTAGTGC  | GGACTACCTG  | AAGTCTGGG  | TGACACTAGG   |
| 239 | ProSerVa    | lThrProAsn | CysLeuAspL  | euArgSerPh | eCysArgAla | AspProLeuC  | ysArgSerAr  | gLeuMetAsp  | PheGlnThrH | isCysHisPro  |
| 901 | TATGGACATC  | CTTGGGACTT | GTGCAACTGA  | GCAGTCCAGA | TGTCTGCGGG | CATACCTGGG  | GCTGATTTGG  | ACTGCCATGA  | CCCCAAACTT | CATCAGCAAG   |
|     | ATACCTGTAG  | GAACCTGAA  | CACGTTGACT  | CGTCAAGTCT | ACAGACGCCC | GTATGACCCC  | CGACTAACCC  | TGACGGTACT  | GGGGTTTGA  | GTAGTCTTC    |
| 272 | MetAspIle   | LeuGlyThrC | ysAlaThrG   | uGlnSerArg | CysLeuArgA | laTyrLeuG   | ylLeulleGly | ThrAlaMetT  | hrProAsnPh | eIleSerLys   |



hGFra3 1 MVRP L N P R P L P P V V L M L L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K  
mGFra3 1 - - M G L S W S P R P P L L M I L L L V L S L W - L P L G A G N S L A T E N R F V N S C T Q A R K K

hGFra3 51 C Q A D P T C S A A Y H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G  
mGFra3 48 C E A N P A C K A A Y Q H L G S C T S S L S R P L P L E E S A M S A D C L E A A E Q L R N S S L I D

hGFra3 101 C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S  
mGFra3 98 C R C H R R M K H Q A T C L D I Y W T V H P A R S L G D Y E L D V S P Y E D T V T S K P W K M N L S

hGFra3 151 K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L  
mGFra3 148 K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H L C L A Q L

hGFra3 201 L T F F E K A A E P H A O G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E  
mGFra3 198 R S F F E K A A E S H A O G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L D

hGFra3 251 L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M  
mGFra3 248 L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M

hGFra3 301 T P N F V S N V N T S V A L S C T C R G S G N L O E E C E M L E G F F S H N P C L T E A I A A K M R  
mGFra3 298 T P N F I S K V N T T V A L S C T C R G S G N L O D E C E Q L E R S F S Q N P C L V E A I A A K M R

hGFra3 351 F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L L S L W  
mGFra3 348 F H R Q L F S Q D W A D S T F S V V Q Q Q N S N P A L R L Q P R L P I L S F S I L P L I L L Q T L W

fig 4

FIGURE 3

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fig 5

48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK  
48614 1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK

48613 51 CQADPTCSAAYHHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG  
48614 51 CQADPTCSAAYHHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRARSL GNYELDVSPYEDTVTSKPWKMNLS  
48614 101 C-M-C-H-R-R-M-K-N-Q-V-A-C-L-D-I-Y-W-T-V-H-R-A-R-S-L . . . . .

48613 151 KLNMLKP DSDLCLKFAMLC TLNDKCDRLRKAYGEACSGPHCQRHVCLRQL  
48614 127 . . . . . DSDLCLKFAMLC TLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTF FEKAAEPHAOGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE  
48614 170 LTF FEKAAEPHAOGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFOTHCHPMDILGTCATEQSRCLRAYLGLIGTAM  
48614 220 LRRLCFSDPLCRSRLVDFOTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR  
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW  
48614 320 FHSQLFSQDWPHPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW

350 300 250 200 150 100 50

FIGURE 4



DNA48613.orf 718 GCGCTGCC...GCTGTGGCCGCCAACTGCCTGGA GCTGCGGCGGCCTCTG  
GDNFRa1.orf 685 TCCTATGAAGAGAGGGAGAAAGCCCAACTGTGTGAATTIGCAGGACTCCTG  
GDNFRa2.orf 724 TCCTATGAAGAGCAAGGAGAAAGCCCAACTGCCTGGA GCTGCGGTGGCGTGTG

DNA48613.orf 765 CTTCCTCCGACCGCTTTGCGAGATCA CGCCTGGTGGATTTCAGACCACT  
GDNFRa1.orf 735 CAAGACGAATTACATCTGCGAGATCTCGCCTTGGCGATTITTTTACCAACT  
GDNFRa2.orf 774 CCGGACTGACCACTGTGTCTGTCTCCGGCTGGCCGACTTCCATGCCAATT

DNA48613.orf 815 GCCATCCCATGGACATCCTAGGAACCTGTGCAACAGAGCAGTCCAGA...  
GDNFRa1.orf 785 GCCAGCCAGAGTCAAGGCTGTGTCAAGCAGCTGTCTAAAGGAATACTACGCT  
GDNFRa2.orf 824 GTCGAGCCTCCTACCAAGAGGTCACCAGCTGCCCTGGGACAATTACCAAG

DNA48613.orf 862 ...TGTCTACGAGCATACCTGGGGCTGATTGGGACTG C CATGACCCCAAA  
GDNFRa1.orf 835 GACTGCTCTCTCGCCTACTCGGGGCTTATTGGCAGAGT CATGACCCCAAA  
GDNFRa2.orf 874 GCGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAA

DNA48613.orf 909 CTTTGT CAGCAATGTCA...ACAC CAGTGTTCCTTTAAGCTGCACT  
GDNFRa1.orf 885 CTACATAGACTCCAGTA...GCTCAGTGTGGCCCATGGTGTGACT  
GDNFRa2.orf 924 CTATGTGACTCCAGCCCACTGGCATCTGTGTGTCCCCCTGGTGCAGCT

DNA48613.orf 953 GCCGAGGCGAGTGGCAACCTGCGAGGAGGAGTGTGAATGCTGGAAAGGGTTC  
GDNFRa1.orf 929 GCAAGCAACAGTGGGAACGACCTAGAAAGAGTGCTTGAAATTCTTGAAATTTC  
GDNFRa2.orf 974 GTCGTGGCAGCGGGAACATGGAGGAGGAGTGTGAGAAGTTCCTCAGGGAC

DNA48613.orf 1003 TTTCTCCCAACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTT  
GDNFRa1.orf 979 TTCAAGGACAAATACATGTCTTAATAAATGCAATTCAAGCCTTTGGCAATGG  
GDNFRa2.orf 1024 TTCACCGAGAACCCATGCCTCCGGAACGCCATCAGGCTTTGGCAACGG

DNA48613.orf 1053 TCA CAGCCA ACTCTTCTCCAGGACTGGCCACACCCCTACCTTTGCTGTGA  
GDNFRa1.orf 1029 CTCCGATGTGACCGTGTGGCAGCCAGCCTTCCAGTACAGACCACCCTG  
GDNFRa2.orf 1074 CACGGACGTGAACGTGTCCCACAAAGGCCCTCTGTTCCAGGCCACCAGG

DNA48613.orf 1103 TGGCACAACCA GAATGAAACCCCTGCTGTGAGGCCACAGCCCTGGGTGCC  
GDNFRa1.orf 1079 CCACTACCACTGTCCTCCGGGTTAAGAACAAACCCCTGGGGCCAGCA  
GDNFRa2.orf 1124 CCCCTCTGGGTGGAAGAGACGCTTCTTTGCCAGATGACCTCAGTGACAGT

DNA48613.orf 1153 TCTCTTTTCTCTGCACTTCTCCCTTGATTCTGCTCTGAGCCTATGGTA  
GDNFRa1.orf 1129 GGGTCTTGAGGAATGAAATCTCCACTCATGTTTGGCCACCGTGTGCAATTIT  
GDNFRa2.orf 1174 ACCAGCTTGGGGACAGTGTCACTACCACTGCACGTCTGTCCAGGAGCA

DNA48613.orf 1203 G...  
GDNFRa1.orf 1179 ACA GGCACAGAAAGCTGAAATCCAAATGTGTGCGGGCAATACACA C CTCTGTA  
GDNFRa2.orf 1224 GGGGCTGAAGGCCAAACAATCCAAAGAGTTAAGCATGTGCTTACAGAGC

GDNFRa1.orf 1229 TTTCCAATGGTAATTATGAATAAGAAAGGTCTCGGTGCTTCCAGCCACATA  
GDNFRa2.orf 1274 TCA CGACAAAATATCATCCCAGGGAGTAACAAGGTGATCAAACCTAACTCA

GDNFRa1.orf 1279 ACCACAATAATCAATGGCTGCTCTCTCAAGCTGTGGTCTGAGCCACCTGCT  
GDNFRa2.orf 1324 GGC CCAAGCAGAGGCCAGACCGTCCGGCTGCCCTGACCGTGTGTCTGCT

GDNFRa1.orf 1329 GGTCTCTGTGGTAAACCGCTCTGTCCACCCTATTATCTTTAACAGAAACAT  
GDNFRa2.orf 1374 GATGCTGAACACAGGCCCTTGTAG

GDNFRa1.orf 1379 CATAG

F16JL5B

DNA48613 1 M V R P L N P R P L P P V V L M L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K  
 GDNFRA1 1 M F L A T . . . L Y F A L . . P L L D L L L S A . . E V S G G D . . . . . R L . . D C V K A S D Q  
 GDNFRA2 1 M I L A N V F C L F F L D E T L R S L A S P S . . S L O G P E L H G W R P P V . . D C V R A N E L

DNA48613 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P . S E E P S V P A D C L E A A Q Q L R N S S L I  
 GDNFRA1 36 C L K E Q S C S T K Y R T L R O C V A G K E T N F S L A S G L E A K D E C R S A M E A L K K K S L Y  
 GDNFRA2 47 C A A E S N C S S R Y R T L R O C L A G R D R N . . . . . T M L A N K E C Q A A L E V L Q E S P L Y

DNA48613 100 G C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L  
 GDNFRA1 86 N C R C K R G M K K E K N C L R I Y W S M Y Q S L . Q G N D L L E D S P Y E P V N S R L S D I F R V  
 GDNFRA2 92 D C R C K R G M K K E L Q C L Q I Y W S I H L G L T E G E E F Y E A S P Y E P V T S R L S D I F R L

DNA48613 150 S K L . . . . . N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S . . . . .  
 GDNFRA1 135 V P F I S . . . V E H I . . P K G N N C L D A A K A C N L D D I C K K Y R S A Y I T P C T T S V S .  
 GDNFRA2 142 A S I F S G T G A D P V V S A K S N H C L D A A K A C N L N D N C K K L R S S Y I S I C N R E I S P

DNA48613 188 G P H C O R H V C L R Q L L T F F E K A A E P H A O G L L L C P C A P N D R G C G E R R R N T I A P  
 GDNFRA1 179 N D V C N R R K C H K A L R Q F F D K V P A K H S Y G M L F C S C . . R D I A C T E R R R O T I V P  
 GDNFRA2 192 T E R C N R R K C H K A L R Q F F D R V P S E Y T Y R M L F C S C . . Q D Q A C A E R R R O T I L P

DNA48613 238 N C A L P P V A . P N C L E L R R L C F S D P L C R S R L V D F O T H C H P . M D I L G T C A T E Q  
 GDNFRA1 227 V C S Y E E R E K P N C L N L Q D S C K T N Y I C R S R L A D F F T N C O P E S R S V S S C L K E N  
 GDNFRA2 240 S C S Y E D K E K P N C L D L R G V C R T D H L C R S R L A D F H A N C R A S Y Q T V T S C P A D N

DNA48613 286 . S R C L R A Y L G L I G T A M T P N F V S N V . . N T S V A L S C T C R G S G N L Q E E C E M L E  
 GDNFRA1 277 Y A D C L L A Y S G L I G T V M T P N Y I D S S . . S L S V A P W C D C S N S G N D L E E C L K F L  
 GDNFRA2 290 Y Q A C L G S Y A G M I G F D M T P N Y V D S S P T G I V V S P W C S C R G S G N M E E E C E K F L

DNA48613 333 G F F S H N P C L T E A I A A . . . . . K M R F H S Q L F S  
 GDNFRA1 325 N F F K D N T C L K N A I Q A F G N G S D V T V W Q P A F P V O T T A T T T T A L R V K N K P L G  
 GDNFRA2 340 R D F T E N P C L R N A I Q A F G N G T D V N V S P K G P S F Q A T Q A P R V E K T P S L P D D L S

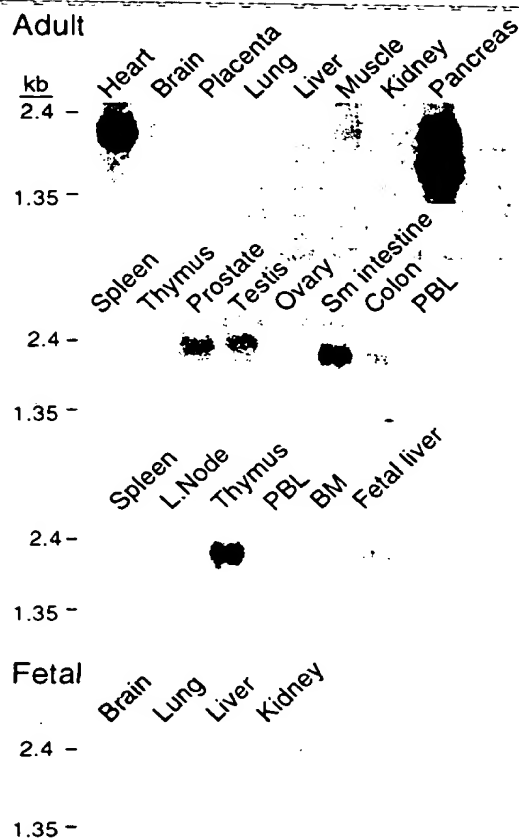
DNA48613 358 Q . . . . . D W P H P T F A V M A H Q N E N P A V R P Q . . . . .  
 GDNFRA1 375 P A G S E N E I P T H V L P P C A N L O A O K L K S N V S G N T H L C I S N G N Y E K E G L G A S S  
 GDNFRA2 390 D S T S . . . L G T S V I T T C T S V Q E Q G L K A N N S K E L S M C F T . . E L T T N I I P G S N

DNA48613 381 . . . . . P W V P S L F S C T L P L I L L L S L W . . . . .  
 GDNFRA1 425 H I T T K S M A A P P S C G L S P L L V L V V T A L S T L L S L T E T S  
 GDNFRA2 435 K V I K P N S G P S R A R P S A A L T V L S V L M L K Q A L . . . . .

# FIGURE 6

protein alignment

666720 220200



NORTHERN BLOTS  
FIGURE 7



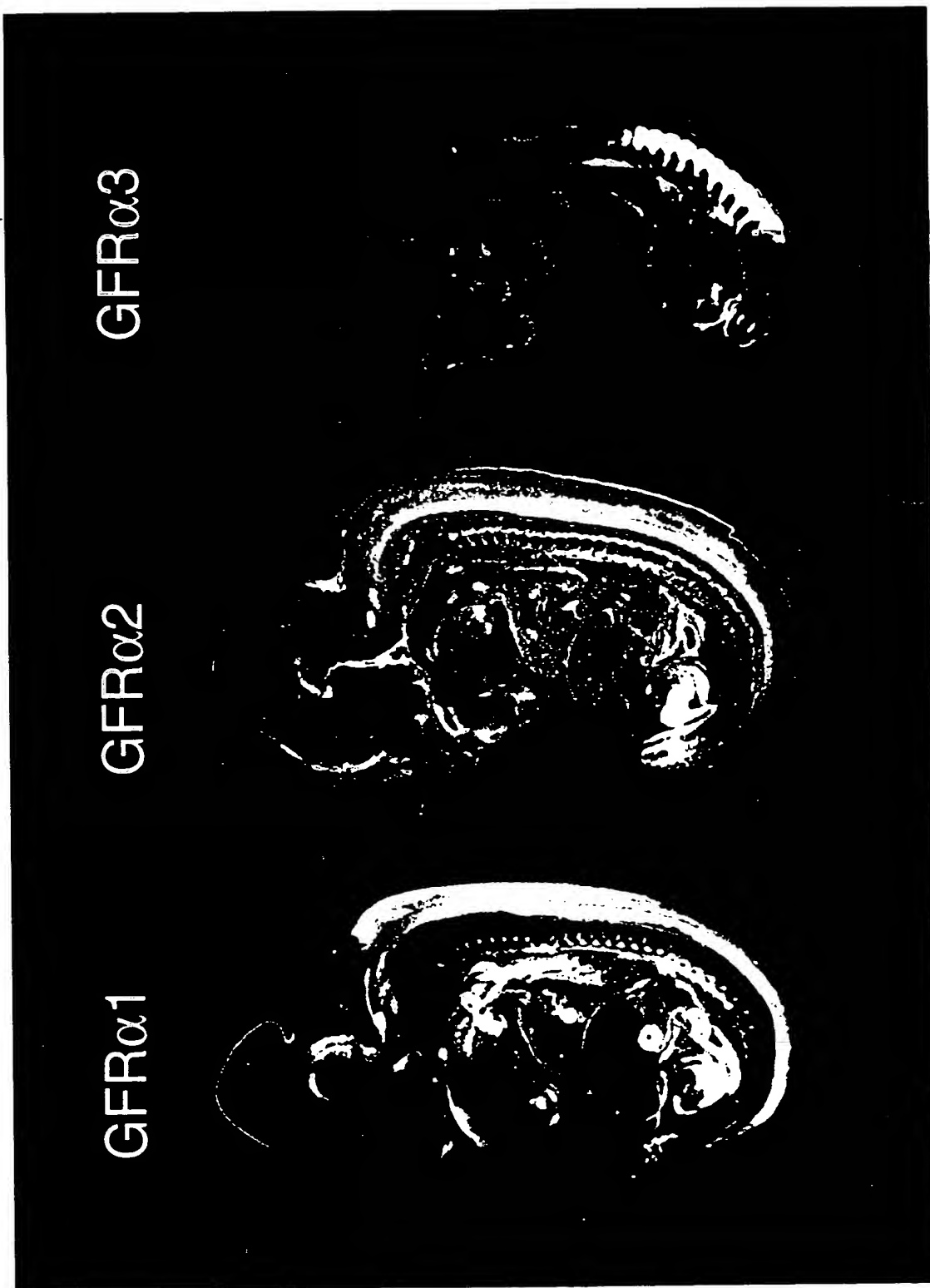


FIGURE 8

FIG. 9A

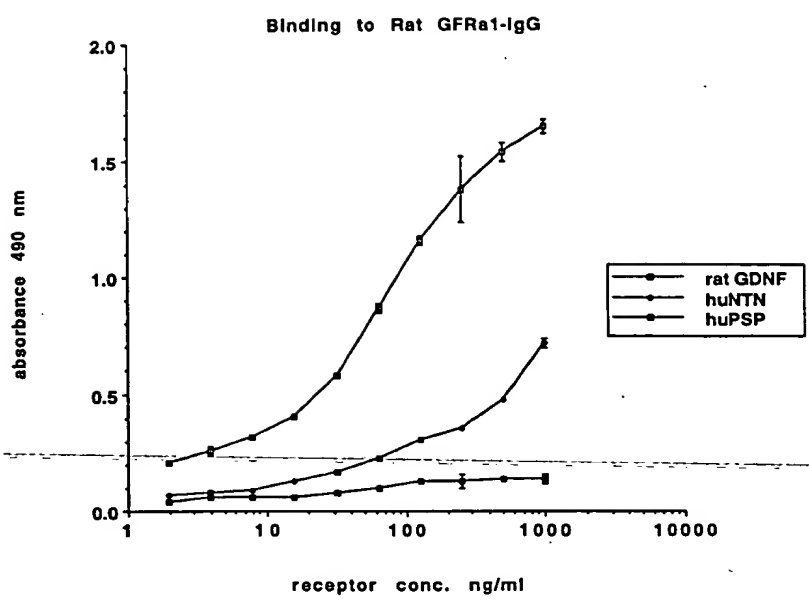


FIG. 9B

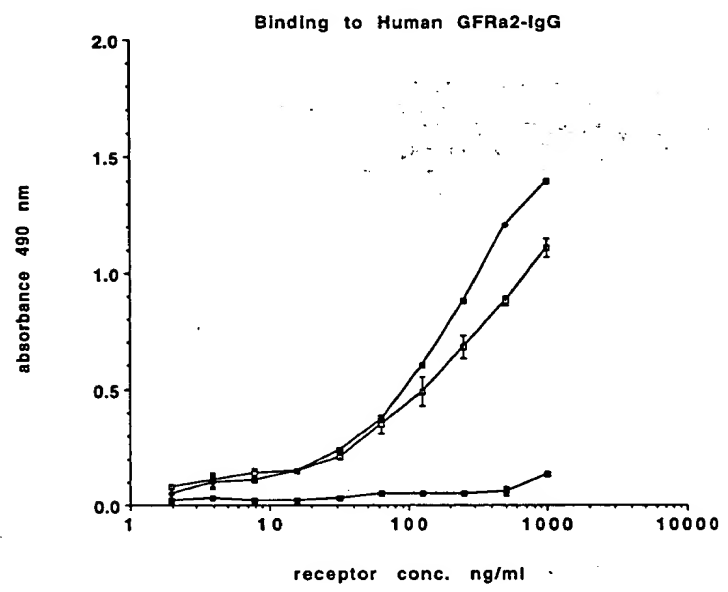
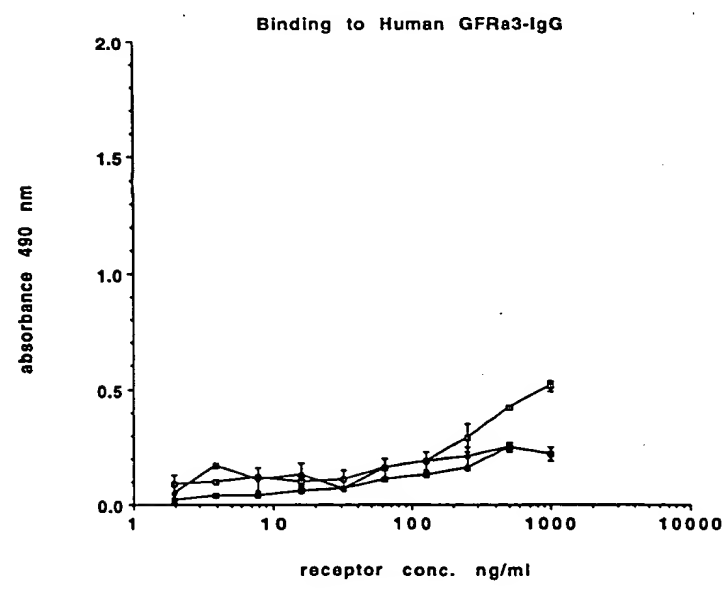


FIG. 9C



2  
Proliferation of Ba/F3-GFRα<sub>3</sub>-mpl cells in response to NTN and GDNF

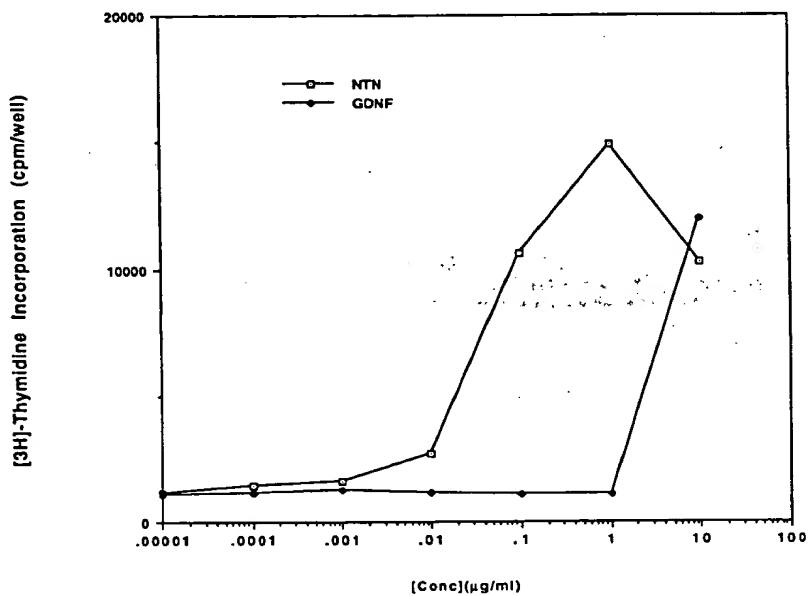


FIGURE 10

Phosphorylation of GFRa2-Rse in response to NTN

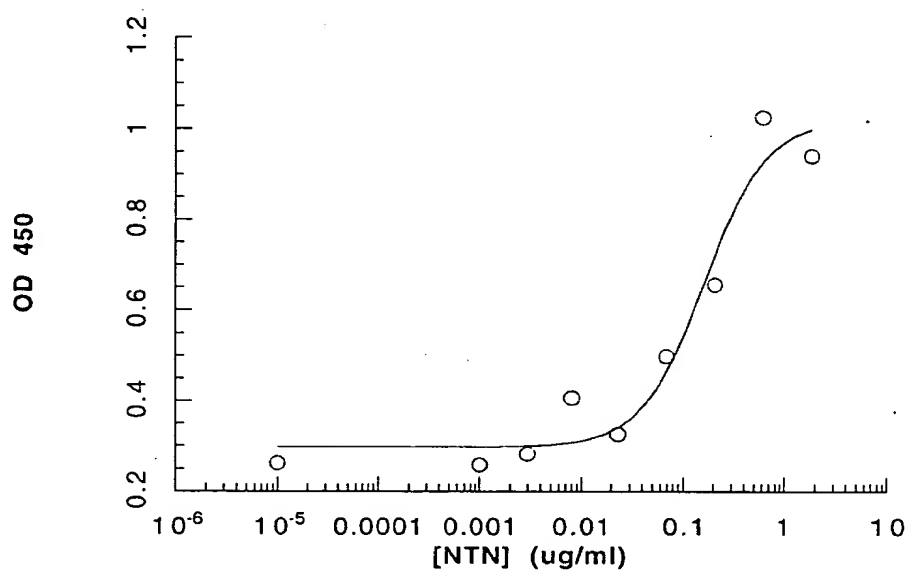


FIGURE 11

Stimulation of GFRa2 and GFRa3 by GDNF, NTN and PSN

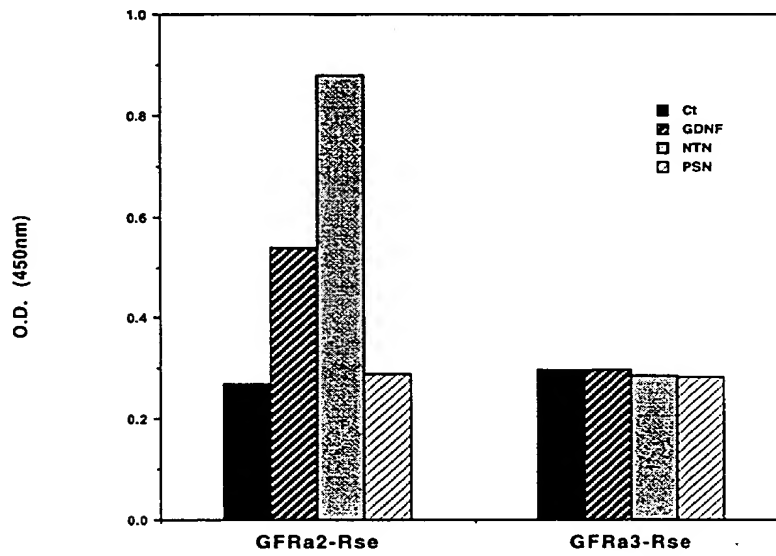
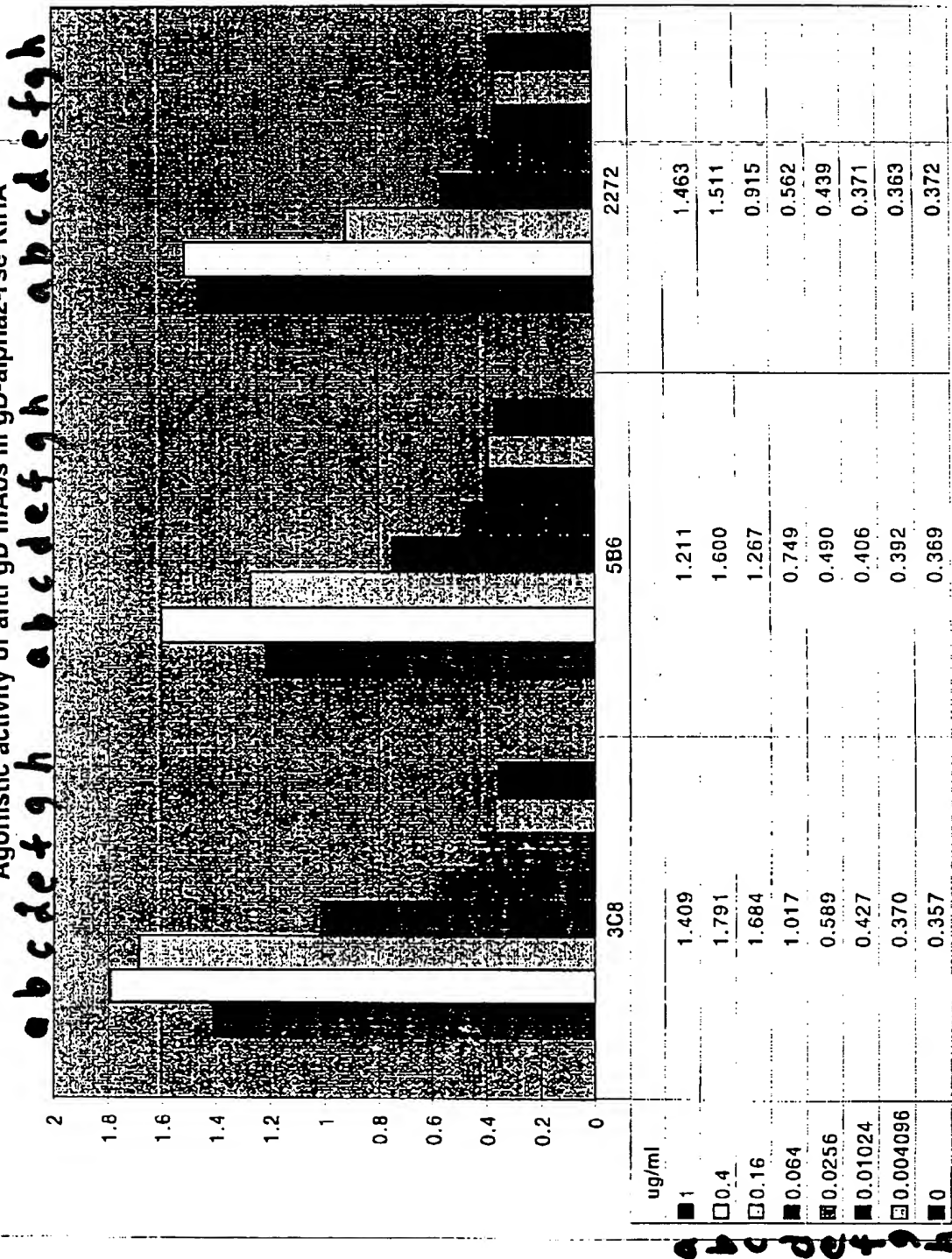


FIGURE 12

# FIGURE 13

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA



1001 GTCAACACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGACAGC TGGAAAAGGTC CTTCTCCCAG AACCCCTGCC  
 CAGTTGTGAT GACAACGGAA TTTCGACGTGG ACGGCTCCGT CGCCGTTGGA TGTCTGCTC ACATTGTCTG ACCTTTCCAG GAAGAGGGTC TTGGGGACGG  
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu  
 1101 TCCTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACACAGCAA  
 AGCACCTCCG GTAACGTCGA TTCTACGCAA AGTGTCTGT CGAGAAAGAGG GTCTGTGATG AAAAAGTCAC CAGCTCGTCG TCTTGTCTGTT  
 339 ValGluAl aileAlaAla LysMetArgp heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn  
 1201 CCCTGTCTCTG AGACTGCAGC CCAGGCTACC CATTTCTTCT TTCTCCATCC TTCCCTTGTAT TCTGTGTCAG ACCCTCTGGT AGCTGGGGCTT CCTCAGGGTC  
 GGGACGAGAC TCTGACGTG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACCTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG  
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuI l eLeuLeuGln ThrLeuTrp  
 1301 CTTTGTCTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGTACAC AGCAACCCCG  
 GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACCTCGGAC ACCACCCCTCT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC  
 1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAACC  
 TTGGTTGGTC CGTAAGGCGT CGTGTAGGCG AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG  
 1501 TCCCTTGCCC CTGCTTCTCTT CTGGCTCAGG CTGGTCTCC TTAGGACTTT TTGGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC  
 AGGGAACGGG GACCAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAG ACAAGACTAC CACTAATCGC CGAGTGGAGG  
 1601 AGCGCTTCTT CCTGTCTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CTTCTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG  
 TCGCGAAGAA GGACAAAGGG TCCTGGTGGG TCCTCGATTC CTTAGTCACT AAGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCTACTGAC  
 1701 AGAAAAATGT TTCTTTTGTG TGGAAAGGCTG GTGCTCCAGC CTCCTGATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC  
 TCCTTTTACA AAGAAACAC ACCTTCCGAC CACGAGGTCG GAGGTGACG GAGACTTACC TTCTATTTTIT GGACGACCAC AGAACTGACG AGACGGTCCG  
 1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCTTAGT CCCTTGGGTC ATGATTAAAC  
 TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGGAACCCAG TACTAATTG  
 1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA  
 TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIGURE 1B